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Nucleotide

Protein

Genome

Structure

PMC

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☐ 1: AJ005830. Escherichia coli ...[gi:3123495]

Links

LOCUS EC05830 2458 bp DNA linear BCT 08-MAR-2000
 DEFINITION Escherichia coli tatABCD operon..
 ACCESSION AJ005830
 VERSION AJ005830.1 GI:3123495
 KEYWORDS mttB gene; mttC gene; Sec-independent protein translocase; tata
 gene; TataA protein; tatB gene; TatB protein; tatC gene; TatC
 protein; tatD gene; TatD protein; yigU gene; yigW gene.
 SOURCE Escherichia coli
 ORGANISM Escherichia coli
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Escherichia.
 REFERENCE 1
 AUTHORS Blattner,F.R., Plunkett,G. III, Bloch,C.A., Perna,N.T., Burland,V.,
 Riley,M., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F.,
 Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J.,
 Mau,B. and Shao,Y.
 TITLE The complete genome sequence of Escherichia coli K-12
 JOURNAL Science 277 (5331), 1453-1474 (1997)
 MEDLINE 97426617
 PUBMED 9278503
 REFERENCE 2
 AUTHORS Sargent,F., Bogsch,E.G., Stanley,N.R., Wexler,M., Robinson,C.,
 Berks,B.C. and Palmer,T.
 TITLE Overlapping functions of components of a bacterial Sec-independent
 protein export pathway
 JOURNAL EMBO J. 17 (13), 3640-3650 (1998)
 MEDLINE 98315056
 PUBMED 9649434
 REFERENCE 3 (bases 1 to 2458)
 AUTHORS Palmer,T.
 TITLE Direct Submission
 JOURNAL Submitted (30-APR-1998) Palmer T., Nitrogen Fixation Laboratory,
 John Innes Centre, NORWICH, NR4 7UH, UNITED KINGDOM
 COMMENT Related sequence: AE000459.
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/citation=[1]

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May 20 2003 11:20:12

have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (<http://cgsc.biology.yale.edu>). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web site (<http://www.genetics.wisc.edu>). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein- or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene names.

FEATURES	Location/Qualifiers
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<u>promoter</u>	27..56 /note="factor Sigma70; predicted +1 start at 4013913"
<u>gene</u>	168..929 /gene="udp" /note="synonym: b3831"
<u>CDS</u>	168..929 /gene="udp" /EC_number="2.4.2.3" /function="enzyme; Salvage of nucleosides and nucleotides" /note="o253; 100 pct identical to UDP_ECOLI SW: P12758" /codon_start=1 /transl_table=11 /product="uridine phosphorylase" /protein_id="AAC76834.1" /db_xref="GI:1790265" /translation="MSKSDVFHLGLTKNDLQGATLAIVPGDPDRVEKIAALMDKPVKL ASHREFTTWRAELDGKPVIVCSTGIGGPSTSIHAVEELAQLGIRTFRLRIGTTGAIQPHI NVGDVLVTTASVRLDGASLHFAPLEFPVADFECTTALVEAAKSIGATTHVGVGTASSD TFYPGQERYDTSGRVVRHFKGSMEEWQAMGVMNYEMESATLLTMCASQGLRAGMVAG VIVNRTQQEIPNAETMKQTESHAVKIVVEAARRLL"
<u>promoter</u>	1009..1037 /note="factor Sigma70; predicted +1 start at 4014894"
<u>gene</u>	1070..2497 /gene="yigN" /note="synonym: b3832"
<u>CDS</u>	1070..2497 /gene="yigN" /function="phenotype; Not classified" /note="o475; 99 pct identical amino acid sequence and equal length to YIGN_ECOLI SW: P27850" /codon_start=1 /transl_table=11

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promoter 2451..2482
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gene 2592..3347
/gene="ubiE"
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Menaquinone, ubiquinone"
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gene complement(8073..8561)
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CDS complement(8073..8561)
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alternate gene names sfrB, hlyT"
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KL"

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promoter 8672..8704
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[NCBI](#) | [NLM](#) | [NIH](#)

May 20 2003 11:20:12

Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (<http://cgsc.biology.yale.edu>). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web site (<http://www.genetics.wisc.edu>). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein- or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene names.

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<u>CDS</u>	176..1834 /gene="citA" /function="putative regulator; Not classified" /note="o552 was o455; This 455 aa ORF is 29 pct identical (15 gaps) to 441 residues of an approx. 544 aa protein YJDH_ECOLI SW: P39272; This 77 aa ORF is 28 pct identical (2 gaps) to 59 residues of an approx. 400 aa protein YWFF_BACSU SW: P39642" /codon_start=1 /transl_table=11 /product="putative sensor-type protein" /protein_id="AAC73720.1" /db_xref="GI:1786837" /translation="MLQLNENKQFAFFQRLAFPLRIFLLILVFSIFVIAALAQYFTAS FEDYLTLHVRDMAMNQAKIIASNDSVISAVKTRDYKRLATIANKLQRTDFDYVVIGD RHSIRLYHPNPEKIGYPMQFTKQGALEKGESYFITGKSGMGMAMRAKTPIFDDDGKVI GVVSIGYLVSKIDSWRAEFLLPMAGVFVLLGILMLLSWFLAAHIRRQMMGMEPKQIA RVVRQQEALFSSVYEGLIAVDPHGYITAINRNARKMLGLSSPGRQWLGKPIVEVVRPA DFFTEQIDEKRQDVVANFNGLSVIANREAIRSGDDLGAIIISFRSKDEISTLNAQLTQ IKQYVESLRTLREHLNWMSTLNGLLQMKEYDRVLAMVQGESQAQQQLIDSLREAFAD RQVAGLLFGKVQRARELGLKMIIVPGSQLSQLPPGLDSTEFAAIVGNLLDNAFEASLR SDEGNKIVELFLSDEGDDVVIEVADQGCVPESLRDKIFEQGVSTRADEPGEHGIGLY LIASYVTRCGGVITLEDNDPCGTLFSIYIPKVKPNDSSINPIDR"
<u>gene</u>	1803..2483 /gene="citB" /note="synonym: b0620"
<u>CDS</u>	1803..2483 /gene="citB" /function="putative regulator; Not classified" /note="o226; 100 pct identical to Shigella flexneri"

protein GB: SFU29654_1 ACCESSION: U29654"
/codon_start=1
/transl_table=11
/product="sequence similarity to Shigella regulator"
/protein_id="AAC73721.1"
/db_xref="GI:1786838"
/translation="MTAPLTLLIVEDETPLAEMHAEYIRHIPGFSQILLAGNLAQARM
MIERFKPGLILLDNYLPDGRGINLLHELVAHYPGDVVFTTAASDMETVSEAVRCGVF
DYLIKPIAYERLGQTLTRFRQRKHMLESIDSASQKQIDEMFNAYARGEKDELPTGID
PLTLNAVRKLFKEPGVQHTAETVAQALTISRRTARRYLEYCASRHLLIAEIVHGKVGR
PQRIYHSG"
gene complement(2524..3909)
/gene="dcuC"
/note="synonym: b0621"
CDS complement(2524..3909)
/gene="dcuC"
/function="transport; Transport of small molecules:
Carbohydrates, organic acids, alcohols"
/note="f461; This 461 aa ORF is 36 pct identical (6 gaps)
to 441 residues of an approx. 456 aa protein YHCL_ECOLI
SW: P45428"
/codon_start=1
/transl_table=11
/product="transport of dicarboxylates"
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/db_xref="GI:1786839"
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AAAAICASPAAILAPTSGDVVLAQAQASEMSLIDFAFKTTLPIISIAAIGMAIAHFFW
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LTIPMLQASNLGRTLSPVSGVVVAVAGMAKISPFEVVKRTSVPVLVGLVIVIVATELM
VPGTAAAVTGK"
promoter complement(3939..3967)
/note="factor Sigma70; predicted +1 start at 655214"
protein_bind complement(4051..4076)
/note="central position to predicted promoter: -107"
/bound_moiety="ArsR predicted site"
promoter 4344..4372
/note="factor Sigma70; predicted +1 start at 655661"
promoter 4443..4471
/note="factor Sigma70; predicted +1 start at 655760"
gene 4498..5058
/gene="crcA"
/note="synonym: b0622"
CDS 4498..5058
/gene="crcA"
/function="orf; Unknown"
/note="o186; 100 pct identical to GB: ECOGICA_1 ACCESSION:
L29054; 100 pct. identical to 156 amino acids of
YBEG_ECOLI SW: P37001 but contains 30 additional
N-terminal residues"
/codon_start=1
/transl_table=11
/product="orf, hypothetical protein"
/protein_id="AAC73723.1"
/db_xref="GI:1786840"
/translation="MNVSKYVAIFSFVFIQLISVGKVFANADEWMTTFRENIAQTWQQ

PEHYDLYIPAITWHARFAYDKEKTDYNERPWGGGFGLSRWDEKGNWHGLYAMAFKDS
WNKWEPIAGYGWESTWRPLADENFHLGLGFTAGVTARDNWNYYIPLPVLLPLASVGYP
VTFQMTYIPGTYNNGNVYFAWMRFQF"

promoter 5084..5112
/note="factor Sigma70; predicted +1 start at 656401"

gene 5233..5442
/gene="cspE"
/note="synonym: b0623"

CDS 5233..5442
/gene="cspE"
/function="phenotype; Not classified"
/note="o69; 100 pct identical to CSPE_ECOLI SW: P36997"
/codon_start=1
/transl_table=11
/product="cold shock protein"
/protein_id="AAC73724.1"
/db_xref="GI:1786841"
/translation="MSKIKGNVWKFNESKGFGFITPEDGSKDVFVHFSAIQTNGFKTL
AECQRVFEFEITNGAKGPSAANVIAL"

gene complement(5496..5879)
/gene="crcB"
/note="synonym: b0624"

CDS complement(5496..5879)
/gene="crcB"
/function="orf; Unknown"
/note="f127; formerly designated ybeI"
/codon_start=1
/transl_table=11
/product="orf, hypothetical protein"
/protein_id="AAC73725.1"
/db_xref="GI:1786842"
/translation="MLQLLLAVFIGGGTGSVARWLLSMRFNPLHQAIPLGTLTANLIG
AFIIGIGFAWFSRMTNIDPVWKVLITTGFCGGLTTFSTFSAEVVFLQLQEGRFWALLN
VFNLLGSFAMTALAFWLFSASTAH"

promoter 5870..5899
/note="factor Sigma70; predicted +1 start at 657188"

promoter complement(5945..5972)
/note="factor Sigma70; predicted +1 start at 657220"

gene 5972..6199
/gene="ybeH"
/note="synonym: b0625"

CDS 5972..6199
/gene="ybeH"
/function="orf; Unknown"
/note="o75; 100 pct identical to YBEH_ECOLI SW: P39874"
/codon_start=1
/transl_table=11
/product="orf, hypothetical protein"
/protein_id="AAC73726.1"
/db_xref="GI:1786843"
/translation="MLVAAGQFAVTSVWEKNAEICASLMAQAAENDASLFALPEALLA
RDDHDADLSVKSAQLLEGEFLGLYGEKVNVT"

gene 6196..6759
/gene="ybeM"
/note="synonym: b0626"

CDS 6196..6759
/gene="ybeM"
/function="putative enzyme; Not classified"
/note="o187; This 187 aa ORF is 40 pct identical (33 gaps)
to 165 residues of an approx. 312 aa protein YJM6_YEAST"

SW: P47016"
/codon_start=1
/transl_table=11
/product="putative amidase"
/protein_id="AAC73727.1"
/db_xref="GI:1786844"
/translation="MMTTILTIHVPSTPGRAWNMLVALQAGNIVARYAKLHLYDAFAI
QESRRVDAGNEIAPLLEVEGMKVGLMTCYDLRFPELALAQALQGAEILVLPAAWVRGP
LKEHHWSTLLAARALDTTCYMVAAGECGNKNIGQSRIIDPFGVTIAAASEMPALIMAE
VTPERVQRVRAQLPVLNNRRFAPPQLL"

promoter 6777..6806
/note="factor Sigma70; predicted +1 start at 658095"

gene 6888..7091
/gene="ybeC"
/note="synonym: b0627"

CDS 6888..7091
/gene="ybeC"
/function="orf; Unknown"
/note="ø67; 98 pct identical to YBEC_ECOLI SW: P25895"
/codon_start=1
/transl_table=11
/product="orf, hypothetical protein"
/protein_id="AAC73728.1"
/db_xref="GI:1786845"
/translation="MGEISITKLLVVAALVVLLFGTKKLRTLGGDLGAAIKGFKKAMN
DDDAAAKKGADVDLQAEKLSHKE"

gene complement(7192..8157)
/gene="lipA"
/note="synonym: b0628"

CDS complement(7192..8157)
/gene="lipA"
/function="putative enzyme; Biosynthesis of cofactors,
carriers: Lipoate"
/note="f321; 99 pct identical to LIPA_ECOLI SW: P25845"
/codon_start=1
/transl_table=11
/product="lipoate synthesis, sulfur insertion?"
/protein_id="AAC73729.1"
/db_xref="GI:1786846"
/translation="MSKPIVMERGVKYRDADKMALIPVKNVATEREALLRKPEWMKIK
LPADSTRIQGIKAAMRKNGLHSVCEEASCPNLAECFNHGTATFMILGAICTRRCPFCD
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PQIKIETLVPDFRGRMDRALDILTATPPDVFNHNLENVPRIYRQVRPGADYNWSLKL
ERFKEAHPEIPTKSGLMVGLGETNEEIIIEVMRDLRRHGVMTLTLGQYLQPSRHLPVQ
RYVSPDEFDEMKAELAMGFTHAACGPFVRSSYHADLQAKGMEVK"

promoter complement(8251..8280)
/note="factor Sigma70; predicted +1 start at 659526"

gene complement(8366..9166)
/gene="ybeF"
/note="synonym: b0629"

CDS complement(8366..9166)
/gene="ybeF"
/function="putative regulator; Not classified"
/note="f266; This 266 aa ORF is 99 pct identical (1 gap)
to 266 residues of an approx. 320 aa protein YBEF_ECOLI
SW: P30979"
/codon_start=1
/transl_table=11
/product="putative transcriptional regulator LYSR-type"
/protein_id="AAC73730.1"

/db_xref="GI:1786847"
/translation="MLNLTPSAISQSIQKLRVIFPDPLFIRKQGQVTPAFAMHLHEY
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SDAENQLSQFQTDLIIDNMFCTNRTVQHHVLFNDNMVLCREGNPLLSLEDDRETIDN
AAHVLLLPPEQNFSGLRQRVQEMFPDRQINFTSYNILTIAALVANSMDLAIIPSRFYN
LFSRCWPLEKLPFPLSLNEEQIDFSIHYNKFSLRDPILHGVIDVIRNAF"
gene complement(9578..10153)
/gene="lipB"
/note="synonym: b0630"
CDS complement(9578..10153)
/gene="lipB"
/function="enzyme; Biosynthesis of cofactors, carriers:
Lipoate"
/note="f191; 99 pct identical to LIPB_ECOLI SW: P30976"
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/product="protein of lipoate biosynthesis"
/protein_id="AAC73731.1"
/db_xref="GI:1786848"
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IQSDRGGQVTYHGPQQVMYVLLNLKRRKLGVRELVTLLLEQTVVNTLAELEGIEAHPRA
DAPGVYVGEKKICSLGLRIRRGCSFHGLALNVNMDLSPFLRINPCGYAGMEMAKISQW
KPEATTNNIAPRLLENILALLNPNDFEYITA"
BASE COUNT 2773 a 2298 c 2547 g 2646 t
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